Project Report: Ecology and Physiology of Permafrost Bacteria

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Project Progress

Specific genes and molecular characteristics required for low–temperature growth can be identified via comparative genomics and are aided by the comparison of close relatives, especially those that come from habitats with important features for discerning cryo–adaptation. We established the growth temperature range of 14 *Psychrobacter* species and identified five distinct growth temperature ranges. Importantly, several *Pschrobacter* species grow at –10 ° C, the lowest temperature tested, and may grow at lower temperatures. We have also isolated at least three different *Psychrobacter* strains from fish in Puerto Rican marine waters and used quantitative PCR to determine the organisms' habitat in Puerto Rico since comparison of strains from a warm environment vs. those from permafrost can reveal genes important to cryo–adaptation . One of the Puerto Rican fish isolates can grow up to 42°C, which would definitely be an interesting strain for genomic comparisons. Real–time PCR revealed that *Psychrobacter* is present in mangrove sediment, suggesting that the presence of this genus is not limited to cold environments and that resistance to desiccation could be an important feature in cold adaptation . The samples were collected during the dry season where the salt precipitates in the sediments and the mean radiation is 600 lengleys.

Physiological, biochemical, 16S rRNA gene and *gyr* B gene phylogenies have been used to resolve the taxonomy and phylogeny of the *Psychrobacter* strains. While most strains are more related to some than others, the phylogeny is not clear. This may have some biological basis reflecting the groups' adaptation to different niches. The genome comparisons should help elucidate the underlying explanation. We have also begun the polyphasic analysis of several *Exiguobacterium* strains including strain 255–15 (whose genome is sequenced), 7–3, and 190–11 isolated from the Siberian permafrost and four other reference strains *E. acetylicum* (DSM20416) , *E. aurantiacum* (DSM6208) , *E. antarcticum* (DSM14480), and *E. undae* (DSM14481). 16S rDNA, DNA–DNA similarity and BOX–PCR demonstrated that the strains 255–15 and 7–3 are closely related and are related to *E. antarcticum* and *E. undae* . DNA–DNA hybridization and the 16S rDNA sequence data show that the strain 190–11 is probably the same species as *E. undae* , which is a strain

isolated in a warmer environment (garden pond in Germany), and hence represents a strain form genomic comparison.

Highlights

- Identified strains of *Psychrobacter* and *Exiguobacterium* from warmer environments that can be used for genomic and proteomic comparisons to help identify traits important to cryo−adaptation.
- Determined that *Psychrobacter* also colonizes salty environments whether warm or frozen, suggesting that adaptation to low water activity may be an important common feature.
- Established the growth temperature range of 14 *Psychrobacter* strains and found that they cover a gradient of temperature ranges and hence are an important resource for resolving temperature adaptation features.

Roadmap Objectives

- ***Objective No. 5.2:*** Co−evolution of microbial communities
- ***Objective No. 5.3:*** Biochemical adaptation to extreme environments
- ***Objective No. 6.2:*** Adaptation and evolution of live beyond Earth